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Gut microbiota composition may relate to weight loss rate in obese pet dogs

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Introduction: The gut microbiota (GM) composition of obese individuals differs from the GM of lean individuals. Furthermore, the efficiency of a high-protein diet to induce weight loss in overweight humans depends on the GM (Santacruz et al. 2009). We aimed to study the interaction between exercise, weight-loss rate and the GM during weight-loss in dogs.

Animals, Material and Methods: Fifteen privately-owned obese dogs were recruited for a 12-week weight-loss intervention, 8 were exercised and fed restrictively with a high-protein diet, while 7 were only fed restrictively and no changes to their exercise regime was made. Fecal samples were collected and the dogs were weighed at baseline, after 6 and 12 weeks (Vitger et al. 2015). GM was determined using MiSeq-based tag-encoded 16S rRNA gene high-throughput amplicon sequencing, and analyzed by ANOVA, ANOSIM and linear regression analyzes (QIIME 1.7.0).

Results and Discussion: Total weight loss, food allowance and GM were not significantly different between groups. Both groups were dominated by genera *Fusobacterium* (~20-50%) and *Bacteroides* (~15-35%). A significant increase in the genera *Suterella*, *Fusobacterium* and a decrease in the *Megamonas* were observed. *Megamonas* abundance negatively correlated to high weight loss (>1% per week). *Ruminococcaceae* were significantly higher at 12 weeks in dogs with a low weight loss (<0.5% per week). Members of *Megamonas* and *Ruminococcaceae* produce acetate, a short chain fatty acid (SCFA), and a substrate for lipogenesis and cholesterol formation (Conterno et al. 2011). Obese rodents also have a GM with a putative increased SCFA producing ability (Turnbaugh et al. 2006), and the GM of some obese individuals may therefore produce more SCFA, which may affect weight loss rate.

Conclusion: Following a 12 week weight-loss intervention in dogs a significant GM change, which may relate to weight loss rate, was seen.

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